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| APPLICATION NO. FILING DATE U97192,579 11/17/98 | MENOZERST NAMED INVE | NTOR | F | ATTORNEY DOCKET NO. |
|---|----------------------|------|--------------|---------------------|
| NIXON AND VANDEHYDE 1100 NORTH GLEBE ROAD | HM32/1129 | | SWART | EXAMINER |
| STH FLOOR ARLINGTON VA 22201 | | | ART QNIT | PAPER NUMBER |
| | | | DATE MAILED: | 11/29/00 |

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks



UNITED STATES DEPARTMENT OF COMMERCE Patent and Trademark Office COMMISSIONER OF PATENTS AND TRADEMARKS

Washington, D.C. 20231

DATE MAILED:

| SERIAL NUMBER | FILING DATE | FIRST NAMED | ATTORNEY DOCKET NO. | |
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| | | | E | EXAMINER |
| • | | | SWARTZ, R | |
| | | | ART UNIT | PAPER NUMBER |
| | | _ [| 1645 | |

Please find below a communication from the EXAMINER in charge of this application

Commissioner of Patents

This Application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR §§ 1.821 - 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequences And/Or Amino Acid Sequence Disclosures.

Any inquiry concerning this communication should be directed to Primary Examiner Rodney P. Swartz, Ph.D., Art Unit 1645, whose telephone number is (703) 308-4244. If unable to reach the examiner, Lynette F. Smith, SPE, can be contacted at (703) 308-43909.

Any questions regarding compliance with the sequence rules requirements specifically should be directed to the departments listed at the bottom of the Notice To Comply.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.F.R. §§ 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Rodney P. Swartz, Ph.D

Primary Examiner Art Unit 1645

November 27, 2000

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CAR §1.821 - §1.825 for the following reasons(s):

| [] | 1. This application clearly fails to comply with the requirements of 37 CAR §1.821 - §1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990, and at 55 FR 18230, May 1, 1990. |
|-----|---|
| [] | 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CAR §1.821(c). |
| [] | 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CAR §1.821(e). |
| [X] | 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CAR §1.822 and/or §1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing". |
| [] | 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CAR §1.825(d). |
| [] | 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CAR §1.821(e). |
| [] | 7. Other: |

APPLICANT MUST PROVIDE:

- [X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- [X] An initial or substitute paper copy of the "Sequence Listing", as were as an amendment directing its entry into the specification.
- [X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CAR §1.821(e) or §1.821(f) or §1.821(g) or §1.825(b) or §1.825(d).

FOR QUESTIONS REGARDING COMPLIANCE WITH THESE REQUIREMENTS, PLEASE CONTACT:

For Rules Interpretation, call (703) 308-1123 For CRF Submission help, call (703)308-4212 For Patentin Software help, call (703) 557-0400

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE.

| | ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/192,577 |
|---------|------------------------------------|--|---|
| ATTN | · NEW DIII ES CASES· P | LEASE DISREGARD ENGLISH "ALPHA" HEADERS, WH | ICH WERE INSERTED BY PTO SOFTWARE |
| 1 | Wrapped Nucleics | The number/text at the end of each line "wrapped" down to | |
| • — | . Wapped Nation | This may occur if your file was retrieved in a word processor | or after creating it. |
| | | Please adjust your right margin to .3, as this will prevent "v | |
| 2 | Wrapped Aminos | The amino acid number/text at the end of each line "wrappe | ed " down to the next line. |
| | **Tapped Allinos | This may occur if your file was retrieved in a word process | |
| | | Please adjust your right margin to .3, as this will prevent "v | |
| 3 | Incorrect Line Length | The rules require that a line not exceed 72 characters in ler | ngth. This includes spaces. |
| 4 | Alicelianced Amine Acid | The numbering under each 5th amino acid is misaligned. T | his may be caused by the use of tabs |
| 4 | Misaligned Amino Acid Numbering | between the numbering. It is recommended to delete any ta | |
| 5 | Non-ASCII | This file was not saved in ASCII (DOS) text, as required by | |
| | | Please ensure your subsequent submission is saved in AS | CII text so that it can be processed. |
| 6 | Variable Length | Sequence(s) contain n's or Xaa's which represented n | |
| | | As per the rules, each n or Xaa can only represent a single | |
| | | Please present the maximum number of each residue having | |
| | | indicate in the (ix) feature section that some may be missing | g. |
| 7 | Patentln ver. 2.0 "bug" | A "bug" in Patentin version 2.0 has caused the <220>-<223 | 3> section to be missing from amino acid |
| | • | sequence(s) Normally, Patentin would aut | |
| | | previously coded nucleic acid sequence. Please manually | |
| | | to the subsequent amino acid sequence. This applies pri | marily to the mandatory <220>-<223> |
| | | sections for Artificial or Unknown sequences. | - de pa |
| ρ | Skipped Sequences | Sequence(s) missing. If intentional, please use the fol | llowing format for each skipped sequence: |
| · | (OLD RULES) | (2) INFORMATION FOR SEQ ID NO:X: | g |
| | (OLD NOLLO) | (i) SEQUENCE CHARACTERISTICS:(Do not insert any h | eadings under "SEQUENCE CHARACTERISTICS") |
| | | (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: | |
| | | This sequence is intentionally skipped | |
| | | Please also adjust the "(iii) NUMBER OF SEQUENCES:" r | esponse to include the skipped sequence(s). |
| 9 | Skipped Sequences | Sequence(s) missing. If intentional, please use the fol | lowing format for each skipped sequence. |
| | (NEW RULES) | <210> sequence id number | • |
| - 1 | | <400> sequence id number | |
| j | | 000 | |
| 10 | Use of n's or Xaa's | Use of n's and/or Xaa's have been detected in the Sequenc | e Listing. |
| | (NEW RULES) | Use of <220> to <223> is MANDATORY if n's or Xaa's are | present. |
| | | In <220> to <223> section, please explain location of n or X | aa, and which residue n or Xaa represents. |
| 11 | Use of <213>Organism | Sequence(s) are missing this mandatory field or it | s response. |
| <u></u> | (NEW RULES) | | |
| | | | • • |
| 12 | Use of <220>Feature | Sequence(s) are missing the <220>Feature and asso | |
| | (NEW RULES) | Use of <220> to <223> is MANDATORY if <213>ORGANI | |
| | | Please explain source of genetic material in <220> to < | |
| | -) (| (See "Federal Register," 6/01/98, Vol. 63, No. | 104, pp. 29031-32) (Sec. 1.823 of new Ru |
| 13 | Patentin ver. 2.0 "bug" | Please do not use "Copy to Disk" function of Patentin | version 2.0. This causes a corrupted |
| | i ateritiri ver. 2.0 bug | file resulting in missing mandatory numeric identifiers and r | |

Instead, please use "File Manager" or any other means to copy file to floppy disk.